

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
- 10 (ii) TITLE OF INVENTION: Apo-2 Receptor
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
20 (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:
- 25 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
- 30 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- 35 (A) NAME: Marschang, Diane L.
(B) REGISTRATION NUMBER: 35,600
(C) REFERENCE/DOCKET NUMBER: P1101R2

(ix) TELECOMMUNICATION INFORMATION:

- 40 (A) TELEPHONE: 650/225-5416
(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 411 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

50 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
1 5 10 15

Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
20 25 30

55 Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
35 40 45

60 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
50 55 60

Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
65 70 75

	Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Glu	Asp	
						80				85				90	
5	Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr
					95					100					105
	His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp
					110					115					120
10	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr
					125					130					135
	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro
					140					145					150
15	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val
					155					160					165
20	Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His
					170					175					180
	Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val
					185					190					195
25	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys
					200					205					210
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp
					215					220					225
30	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp
					230					235					240
35	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val
					245					250					255
	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly
					260					265					270
40	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro
					275					280					285
	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala
					290					295					300
45	Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp
					305					310					315
	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg
50					320					325					330
	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu
					335					340					345
55	Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp
					350					355					360
	Val	Asn	Lys	Thr	Gly	Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp
					365					370					375
60	Ala	Leu	Glu	Thr	Leu	Gly	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu
					380					385					390
	Asp	His	Leu	Leu	Ser	Ser	Gly	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn

Ala Asp Ser Ala Xaa Ser
410 411

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15

CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT 50

GCGCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC 100

20

CCACGGGCCT GAGAGACTAT AAGAGCGTTC CCTACCGCC ATG GAA 145
Met Glu
1

25

CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG GCC CGG 184
Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
5 10 15

30

AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC 223
Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala
20 25

35

AGG CCT GGG CTC CGG GTC CCC AAG ACC CTT GTG CTC GTT 262
Arg Pro Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val
30 35 40

GTC GCC GCG GTC CTG CTG TTG GTC TCA GCT GAG TCT GCT 301
Val Ala Ala Val Leu Leu Leu Val Ser Ala Glu Ser Ala
45 50

40

CTG ATC ACC CAA CAA GAC CTA GCT CCC CAG CAG AGA GCG 340
Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln Gln Arg Ala
55 60 65

45

GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA GAG GGA TTG 379
Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
70 75 80

50

TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT 418
Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
85 90

55

TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC 457
Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His
95 100 105

60

TGG AAT GAC CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT 496
Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys
110 115

GAT TCA GGT GAA GTG GAG CTA AGT CCC TGC ACC ACG ACC 535
Asp Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr
120 125 130

10052798-110304

P1101R2

	AGA	AAC	ACA	GTG	GTG	CAG	TGC	GAA	GAA	GGC	ACC	TTC		574
	Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
			135					140					145	
5	GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
	Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
					150					155				
10	GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	652
	Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	
		160				165						170		
15	CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
				175					180					
20	ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
					185		190				195			
25	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
			200					205					210	
30	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
					215				220					
35	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
		225					230					235		
40	GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
	Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
				240				245						
45	TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
	Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
		250				255					260			
50	CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
			265					270					275	
55	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	GCA	GAA	GCT	1003
	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	Ala	Glu	Ala	
					280				285					
60	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	1042
	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	
		290					295					300		
65	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	1081
	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	
				305				310						
70	GAC	TTT	GCA	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	1120
	Asp	Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	
		315				320					325			
75	CTC	ATG	AGG	AAG	TTG	GGC	CTC	ATG	GAC	AAT	GAG	ATA	AAG	1159
	Leu	Met	Arg	Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	
			330				335					340		

P1101R2

GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC 1198
Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
345 350

5 TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237
Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg
355 360 365

10 GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276
Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr
370 375

15 CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315
Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His
380 385 390

20 TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354
Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400
Ala Asp Ser Ala Xaa Ser
410 411

25 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450

AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500

30 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTTACTGCAC 1550

TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600

GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTGGT TGGGATGTCA 1650

35 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700

TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750

40 GCGGCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 70 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50

GCTAAAGCTG AGGCAGCGGG 70

55

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 29 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:



10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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(2) INFORMATION FOR SEQ ID NO:6:

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30 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
35 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro-Leu-Val-Val-Pro-Phe-Tyr-Ala-Ala-Gln-Pro-Ala-Met
30 35

[illegible]

45 CGG CCG GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
Arg Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
55 60

50 GGA TTC ACC TTT GAT GAT TAT GGC ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Asp Asp Tyr Gly Met Ser Trp Val Arg
 65 70 75

CAA GCT CCA GGG AAG GGG CTG GAG TGG GTC TCT GGT ATT 270
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile
55 80 85 90

AAT TGG AAT GGT GGT AGC ACA GGA TAT GCA GAC TCT GTG 309
Asn Trp Asn Gly Gly Ser Thr Gly Tyr Ala Asp Ser Val
95 100

60
AAG GGC CGA GTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ala Lys Asn
105 110 115

TCC CTG TAT CTG AATG AAC AGC CTG AGA GCC GAG 387
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

5 ACG GCC GTA TAT TAC TGT GCG AAA ATC CTG GGT GCC GGA 426
 Thr Ala Val Tyr Tyr Cys Ala Lys Ile Leu Gly Ala Gly
 130 135 140

10 CGG GGC TGG TAC TTC GAT CTC TGG GGG AAG GGG ACC ACG 465
 Arg Gly Trp Tyr Phe Asp Leu Trp Gly Lys Gly Thr Thr
 145 150 155

15 GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA GGC GGA GGT 504
 Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 160 165

20 GGC AGC GGC GGT GGC GGA TCG TCT GAG CTG ACT CAG GAC 543
 Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln Asp
 170 175 180

CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA GTC AGG ATC 582
 Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile
 185 190

25 ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA AGC 621
 Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 195 200 205

30 TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC 660
 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val
 210 215 220

35 ATC TAT GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC 699
 Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp
 225 230

CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA GCT TCC TTG 738
 Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu
 235 240 245

40 ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG GCT GAC TAT 777
 Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr
 250 255

45 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
 260 265 270

50 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 275 280 285

55 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894
 Ala His His His His His His Gly Ala Ala Glu Gln Lys
 290 295

CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 300 305 309

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
 10 1 5 10

TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
 15 15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met
 30 35

GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val
 40 45 50

CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg
 30 65 70 75

CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
 80 85 90

AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309
 Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 95 100

AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 105 110 115

TCA CTG TAT CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC 387
 Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

ACG GCT GTG TAT TAC TGT GCG AGA GAT CTT TTA AAG GTC 426
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Leu Lys Val
 50 130 135 140

AAG GGC AGC TCG TCT GGG TGG TTC GAC CCC TGG GGG AGA 465
 Lys Gly Ser Ser Ser Gly Trp Phe Asp Pro Trp Gly Arg
 145 150 155

GGG ACC ACG GTC ACC GTC TCG AGT GGT GGA GGC GGT TCA 504
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
 160 165

GGC GGA GGT GGT AGC GGC GGT GGC GGA TCG TCT GAG CTG 543
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu
 170 175 180

ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG ACA 582

Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
185 190

5 GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT 621
Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr
195 200 205

10 TAT GCA AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT 660
Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro
210 215 220

15 GTA CTT GTC ATC TAT GGT AAA AAC AAC CCG CCC TCA GGG 699
Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly
225 230

20 ATC CCA GAC CGA TTC TCT GGC TCC AGC TCA GGA AAC ACA 738
Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr
235 240 245

25 GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA GAT GAG 777
Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu
250 255

30 GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC 816
Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn
260 265 270

35 CAT GTG GTA TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA 855
His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
275 280 285

40 GGT GCG GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA 894
Gly Ala Ala Ala His His His His His His Gly Ala Ala
290 295

45 GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC 933
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala
300 305 310

40 GCA TAG 939
Ala
312

(2) INFORMATION FOR SEQ ID NO:8:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 933 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36
Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe
1 5 10

60 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75
Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile
15 20 25

CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114
Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met

5 GCC CAG GTG CAG CTG GTG CAG TCT GGG GGA GGC GTG GTC 153
 Ala Gln Val Gln Leu Val Gln Ser Gly Gly Gly Val Val
 40 45 50

10 CAG CCT GGG CGG TCC CTG AGA CTC TCC TGT GCA GCT TCT 192
 Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
 55 60

15 GGG TTC ATT TTC AGT AGT TAT GGG ATG CAC TGG GTC CGC 231
 Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp Val Arg
 65 70 75

20 CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG GCA GGT ATT 270
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Gly Ile
 80 85 90

25 TTT TAT GAT GGA GGT AAT AAA TAC TAT GCA GAC TCC GTG 309
 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val
 95 100

30 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC 348
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
 105 110 115

35 ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC 387
 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 120 125

40 ACG GCT GTG TAT TAC TGT GCG AGA GAT AGG GGC TAC TAC 426
 Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Tyr Tyr
 130 135 140

45 TAC ATG GAC GTC TGG GGC AAA GGG ACC ACG GTC ACC GTC 465
 Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val
 145 150 155

50 TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504
 Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 160 165

55 GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543
 Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser
 170 175 180

60 GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582
 Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys
 185 190

65 ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621
 Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val
 195 200 205

70 CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660
 His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
 210 215 220

75 CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699
 Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro
 225 230

80 GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738
 Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser

245

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25 (2) INFORMATION FOR SEQ ID NO:9:

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Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser

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160

165

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Leu Thr Gln
 170 175 180
 5 Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
 185 190 195
 10 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln
 200 205 210
 Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn
 215 220 225
 15 Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser
 230 235 240
 Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp
 245 250 255
 20 Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
 260 265 270
 25 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala
 275 280 285
 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
 290 295 300
 30 Ser Glu Glu Asp Leu Asn Gly Ala Ala
 305 309

(2) INFORMATION FOR SEQ ID NO:10:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1 5 10 15
 45 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 25 30
 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gly Val Gln Leu Val Glu
 35 40 45
 50 Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
 50 55 60
 55 Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp
 65 70 75
 Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile
 80 85 90
 60 Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys Gly
 95 100 105
 Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 110 115 120

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135
 5 Ala Arg Asp Leu Leu Lys Val Lys Gly Ser Ser Ser Gly Trp Phe
 140 145 150
 Asp Pro Trp Gly Arg Gly Thr Thr Val Thr Val Ser Ser Gly Gly
 155 160 165
 10 Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu
 170 175 180
 Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val
 185 190 195
 15 Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser
 200 205 210
 20 Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 215 220 225
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly
 230 235 240
 25 Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln
 245 250 255
 Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser
 260 265 270
 30 Gly Asn His Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
 275 280 285
 35 Gly Ala Ala Ala His His His His His His Gly Ala Ala Glu Gln
 290 295 300
 Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 305 310 312

40

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

50 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile
 1 5 10 15
 Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro
 20 25 30
 55 Phe Tyr Ala Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln
 35 40 45
 Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser
 50 55 60
 Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met His Trp
 65 70 75

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Ile
 80 85 90
 5 Phe Tyr Asp Gly Gly Asn Lys Tyr Tyr Ala Asp Ser Val Lys Gly
 95 100 105
 Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 110 115 120
 10 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 125 130 135
 Ala Arg Asp Arg Gly Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly
 140 145 150
 15 Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 155 160 165
 20 Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro
 170 175 180
 Ser Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr
 185 190 195
 25 Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val His Trp Tyr
 200 205 210
 Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Asp Asp
 215 220 225
 30 Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Arg
 230 235 240
 35 Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln Ala Glu
 245 250 255
 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg
 260 265 270
 40 Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala
 275 280 285
 Ala Ala His His His His His Gly Ala Ala Glu Gln Lys Leu
 290 295 300
 45 Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 305 310

(2) INFORMATION FOR SEQ ID NO:12:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

-55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

60

AGCGGATAAC AATTCACAC AGG 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGAGGGTAG T 21

10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

20

Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu
1 5 10 12

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